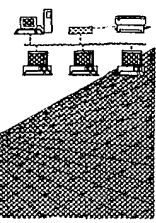


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BIOTECHNOLOGY  
JUN 24 2003  
SYSTEMS  
BRANCH

TECH CENTER 1600/2000



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/165,546B  
Source: 1600  
Date Processed by STIC: 6/18/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/165546B
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

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Page 1 of 4

JUN 24 2003

TECH CENTER 1600/2910



1600

RAW SEQUENCE LISTING

DATE: 06/18/2003

PATENT APPLICATION: US/09/165,546B

TIME: 11:50:17

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\06182003\I165546B.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

C--> 2 (i) APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,  
3 Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd  
5 (ii) TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO  
6 AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO  
7 MHC CLASS I AND MHC CLASS II MOLECULES, AND  
8 USES THEREOF

10 (iii) NUMBER OF SEQUENCES: 15

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: FULBRIGHT & JAWORSKI LLP  
14 (B) STREET: 666 Fifth Avenue  
15 (C) CITY: New York City  
16 (D) STATE: New York  
17 (E) COUNTRY: USA  
18 (F) ZIP: 10158

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
22 (B) COMPUTER: IBM  
23 (C) OPERATING SYSTEM: PC-DOS  
24 (D) SOFTWARE: WordPerfect

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/165,546B  
C--> 28 (B) FILING DATE: 02-Oct-1998  
29 (C) CLASSIFICATION: 530

39 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 08/937,263  
33 (B) FILING DATE: April 17, 1998  
36 (A) APPLICATION NUMBER: 08/937,263  
37 (B) FILING DATE: September 15, 1997  
40 (A) APPLICATION NUMBER: US 08/752,182  
41 (B) FILING DATE: 03-October-1996

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Hanson, Norman D.  
45 (B) REGISTRATION NUMBER: 30,946  
46 (C) REFERENCE/DOCKET NUMBER: LUD 5466.3

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (212) 688-9200  
50 (B) TELEFAX: (212) 838-3884

*pp 1-3*  
Does Not Comply  
Corrected Diskette Needed

*already  
delete - shown below  
with correct filing date*

ERRORED SEQUENCES

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/165,546B

DATE: 06/18/2003  
TIME: 11:50:17

Input Set : A:\pto.da.txt  
Output Set: N:\CRF4\06182003\I165546B.raw

130 (2) INFORMATION FOR SEQ ID NO: 3:  
131 (i) SEQUENCE CHARACTERISTICS:  
132 (A) LENGTH: 32 base pairs  
E--> 133 (B) TYPE: nuclear acid *nucleic acid This is a global error.*  
134 (C) STRANDEDNESS: single  
135 (D) TOPOLOGY: linear  
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
138 CACACAAAGC TTGGCTTAGC GCCTCTGCCC TG 32  
274 (2) INFORMATION FOR SEQ ID NO: 15:  
275 (i) SEQUENCE CHARACTERISTICS:  
276 (A) LENGTH: 180 amino acids  
277 (B) TYPE: amino acid  
278 (D) TOPOLOGY: linear  
279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15  
E--> 281 Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala  
282 5 ~~10~~ 10 15 15 ← misaligned NOS.  
283 Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn  
284 20 25 30 do not use TAB  
E--> 285 Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Ala Pro invalid codes between  
286 35 40 45 numbers  
287 Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Ala  
288 50 55 60  
289 Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys  
290 65 70 75  
291 Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe  
292 80 85 90  
293 Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala  
294 95 100 105  
295 Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly  
296 110 115 120  
297 Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile  
298 125 130 135  
299 Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser  
300 140 145 150  
301 Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys  
302 155 160 165  
303 Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg  
304 170 175 180  
306 25303395\_1.DOC -1-

from sequence 1.

09/165,546B

3

ATCCTCGTGG GCCCTGACCT TCTCTCTGAG AGCCGGGCAG AGGCTCCGGA GCC	53
ATG CAG GCC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT	98
Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala	
5 10 15 15	
GAT GGC CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT	143
Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn	
20 25 30 30	
GCT GGC GGC CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC	188
Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg (Ala) Pro	
35 40 40 45 45	

↓  
invalid

sample of misaligned amino acid nos.

see item 3 on Error Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/165,546B

DATE: 06/18/2003

TIME: 11:50:18

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\06182003\I165546B.raw

L:2 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]  
 L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
 L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:132 M:241 E: Invalid Alpha Header Field, [TYPE:], SeqNo=3  
 L:188 M:220 C: Keyword misspelled or invalid format, [(i) SEQUENCE CHARACTERISTICS:]  
 L:282 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15  
 L:285 M:330 E: (2) Invalid Amino Acid Designator, 1